

SEQUENCE LISTING

<110> Olmsted, Robert  
Keith, Paula  
Dryga, Sergey  
Caley, Ian  
Maughan, Maureen  
Johnston, Robert  
Davis, Nancy  
Swanstrom, Ronald

<120> ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE AS VACCINES

<130> 01113.0001U3

<150> 09/902,537

<151> 2001-07-09

<150> 60/216,995

<151> 2000-07-07

<160> 19

<170> FastSEQ for Windows Version 4.0

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<211> 12523

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence; Note =  
synthetic construct

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tggcaaagggt	agcgttgcca	atgatgttac	agatgagatg	gtcagactaa	actggctgac	11760
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actcaccact	gcgatccccg	ggaaaacagc	attccaggta	ttagaagaat	atcctgattc	11880
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cggtgagttt	tctccttcat	tacagaaacg	gctttttcaa	aaatatggta	ttgataatcc	12300
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gcagtcaggc	accgtgtatg	aaatctaaca	atgcgtcat	cgtcatcctc	ggcaccgtca	12480
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<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

<221> CDS  
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Met	Glu	Lys	Val	His	Val	Asp	Ile	Glu	Glu	Asp	Ser	Pro	Phe	Leu	Arg	
1				5				10						15		

gct ttg cag cgg agc ttc ccg cag ttt gag gta gaa gcc aag cag gtc															96	
Ala	Leu	Gln	Arg	Ser	Phe	Pro	Gln	Phe	Glu	Val	Glu	Ala	Lys	Gln	Val	
			20					25					30			

act gat aat gac cat gct aat gcc aga gcg ttt tcg cat ctg gct tca															144	
Thr	Asp	Asn	Asp	His	Ala	Asn	Ala	Arg	Ala	Phe	Ser	His	Leu	Ala	Ser	
		35					40				45					

aaa ctg atc gaa acg gag gtg gac cca tcc gac acg atc ctt gac att															192	
Lys	Leu	Ile	Glu	Thr	Glu	Val	Asp	Pro	Ser	Asp	Thr	Ile	Leu	Asp	Ile	
		50				55				60						

gga agt gcg ccc gcc cgc aga atg tat tct aag cac aag tat cat tgt															240	
Gly	Ser	Ala	Pro	Ala	Arg	Arg	Met	Tyr	Ser	Lys	His	Lys	Tyr	His	Cys	
	65				70				75					80		

atc tgt ccg atg aga tgt gcg gaa gat ccg gac aga ttg tat aag tat															288	
Ile	Cys	Pro	Met	Arg	Cys	Ala	Glu	Asp	Pro	Asp	Arg	Leu	Tyr	Lys	Tyr	
				85				90						95		

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gca act aag ctg aag aaa aac tgt aag gaa ata act gat aag gaa ttg	336
Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu	
100 105 110	
gac aag aaa atg aag gag ctc gcc gcc gtc atg agc gac cct gac ctg	384
Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu	
115 120 125	
gaa act gag act atg tgc ctc cac gac gac gag tcg tgt cgc tac gaa	432
Glu Thr Glu Thr Met Cys Leu His Asp Asp Glu Ser Cys Arg Tyr Glu	
130 135 140	
ggg caa gtc gct gtt tac cag gat gta tac gcg gtt gac gga ccg aca	480
Gly Gln Val Ala Val Tyr Gln Asp Val Tyr Ala Val Asp Gly Pro Thr	
145 150 155 160	
agt ctc tat cac caa gcc aat aag gga gtt aga gtc gcc tac tgg ata	528
Ser Leu Tyr His Gln Ala Asn Lys Gly Val Arg Val Ala Tyr Trp Ile	
165 170 175	
ggc ttt gac acc acc cct ttt atg ttt aag aac ttg gct gga gca tat	576
Gly Phe Asp Thr Thr Pro Phe Met Phe Lys Asn Leu Ala Gly Ala Tyr	
180 185 190	
cca tca tac tct acc aac tgg gcc gac gaa acc gtg tta acg gct cgt	624
Pro Ser Tyr Ser Thr Asn Trp Ala Asp Glu Thr Val Leu Thr Ala Arg	
195 200 205	
aac ata ggc cta tgc agc tct gac gtt atg gag cgg tca cgt aga ggg	672
Asn Ile Gly Leu Cys Ser Ser Asp Val Met Glu Arg Ser Arg Arg Gly	
210 215 220	
atg tcc att ctt aga aag aag tat ttg aaa cca tcc aac aat gtt cta	720
Met Ser Ile Leu Arg Lys Lys Tyr Leu Lys Pro Ser Asn Asn Val Leu	
225 230 235 240	
ttc tct gtt ggc tcg acc atc tac cac gag aag agg gac tta ctg agg	768
Phe Ser Val Gly Ser Thr Ile Tyr His Glu Lys Arg Asp Leu Leu Arg	
245 250 255	
agc tgg cac ctg ccg tct gta ttt cac tta cgt ggc aag caa aat tac	816
Ser Trp His Leu Pro Ser Val Phe His Leu Arg Gly Lys Gln Asn Tyr	
260 265 270	
aca tgt cgg tgt gag act ata gtt agt tgc gac ggg tac gtc gtt aaa	864
Thr Cys Arg Cys Glu Thr Ile Val Ser Cys Asp Gly Tyr Val Val Lys	
275 280 285	
aga ata gct atc agt cca ggc ctg tat ggg aag cct tca ggc tat gct	912
Arg Ile Ala Ile Ser Pro Gly Leu Tyr Gly Lys Pro Ser Gly Tyr Ala	
290 295 300	
gct acg atg cac cgc gag gga ttc ttg tgc tgc aaa gtg aca gac aca	960
Ala Thr Met His Arg Glu Gly Phe Leu Cys Cys Lys Val Thr Asp Thr	
305 310 315 320	

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tta aac ggg gag agg gtc tct ttt ccc gtg tgc acg tat gtg cca gct	1008
Leu Asn Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ala	
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aca ttg tgt gac caa atg act ggc ata ctg gca aca gat gtc agt gcg	1056
Thr Leu Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Ala	
340 345 350	
gac gac gcg caa aaa ctg ctg gtt ggg ctc aac cag cgt ata gtc gtc	1104
Asp Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val	
355 360 365	
aac ggt cgc acc cag aga aac acc aat acc atg aaa aat tac ctt ttg	1152
Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu Leu	
370 375 380	
ccc gta gtg gcc cag gca ttt gct agg tgg gca aag gaa tat aag gaa	1200
Pro Val Val Ala Gln Ala Phe Ala Arg Trp Ala Lys Glu Tyr Lys Glu	
385 390 395 400	
gat caa gaa gat gaa agg cca cta gga cta cga gat aga cag tta gtc	1248
Asp Gln Glu Asp Glu Arg Pro Leu Gly Leu Arg Asp Arg Gln Leu Val	
405 410 415	
atg ggg tgt tgt tgg gct ttt aga agg cac aag ata aca tct att tat	1296
Met Gly Cys Cys Trp Ala Phe Arg Arg His Lys Ile Thr Ser Ile Tyr	
420 425 430	
aag cgc ccg gat acc caa acc atc atc aaa gtg aac agc gat ttc cac	1344
Lys Arg Pro Asp Thr Gln Thr Ile Ile Lys Val Asn Ser Asp Phe His	
435 440 445	
tca ttc gtg ctg ccc agg ata ggc agt aac aca ttg gag atc ggg ctg	1392
Ser Phe Val Leu Pro Arg Ile Gly Ser Asn Thr Leu Glu Ile Gly Leu	
450 455 460	
aga aca aga atc agg aaa atg tta gag gag cac aag gag ccg tca cct	1440
Arg Thr Arg Ile Arg Lys Met Leu Glu Glu His Lys Glu Pro Ser Pro	
465 470 475 480	
ctc att acc gcc gag gac gta caa gaa gct aag tgc gca gcc gat gag	1488
Leu Ile Thr Ala Glu Asp Val Gln Glu Ala Lys Cys Ala Ala Asp Glu	
485 490 495	
gct aag gag gtg cgt gaa gcc gag gag ttg cgc gca gct cta cca cct	1536
Ala Lys Glu Val Arg Glu Ala Glu Glu Leu Arg Ala Ala Leu Pro Pro	
500 505 510	
ttg gca gct gat gtt gag gag ccc act ctg gaa gcc gat gtc gac ttg	1584
Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu	
515 520 525	
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Met Leu Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly Leu	
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Ile Lys Val Thr Ser Tyr Ala Gly Glu Asp Lys Ile Gly Ser Tyr Ala	
545 550 555 560	
gtg ctt tct ccg cag gct gta ctc aag agt gaa aaa tta tct tgc atc	1728
Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile	
565 570 575	
cac cct ctc gct gaa caa gtc ata gtg ata aca cac tct ggc cga aaa	1776
His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys	
580 585 590	
ggg cgt tat gcc gtg gaa cca tac cat ggt aaa gta gtg gtg cca gag	1824
Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu	
595 600 605	
gga cat gca ata ccc gtc cag gac ttt caa gct ctg agt gaa agt gcc	1872
Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala	
610 615 620	
acc att gtg tac aac gaa cgt gag ttc gta aac agg tac ctg cac cat	1920
Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His	
625 630 635 640	
att gcc aca cat gga gga gcg ctg aac act gat gaa gaa tat tac aaa	1968
Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys	
645 650 655	
act gtc aag ccc agc gag cac gac ggc gaa tac ctg tac gac atc gac	2016
Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp	
660 665 670	
agg aaa cag tgc gtc aag aaa gaa cta gtc act ggg cta ggg ctc aca	2064
Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr	
675 680 685	
ggc gag ctg gtg gat cct ccc ttc cat gaa ttc gcc tac gag agt ctg	2112
Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu	
690 695 700	
aga aca cga cca gcc gct cct tac caa gta cca acc ata ggg gtg tat	2160
Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr	
705 710 715 720	
ggc gtg cca gga tca ggc aag tct ggc atc att aaa agc gca gtc acc	2208
Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr	
725 730 735	
aaa aaa gat cta gtg gtg agc gcc aag aaa gaa aac tgt gca gaa att	2256
Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile	
740 745 750	
ata agg gac gtc aag aaa atg aaa ggg ctg gac gtc aat gcc aga act	2304
Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr	
755 760 765	

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Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu	
770 775 780	
tat att gac gaa gct ttt gct tgt cat gca ggt act ctc aga gcg ctc	2400
Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu	
785 790 795 800	
ata gcc att ata aga cct aaa aag gca gtg ctc tgc ggg gat ccc aaa	2448
Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys	
805 810 815	
cag tgc ggt ttt ttt aac atg atg tgc ctg aaa gtg cat ttt aac cac	2496
Gln Cys Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His	
820 825 830	
gag att tgc aca caa gtc ttc cac aaa agc atc tct cgc cgt tgc act	2544
Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr	
835 840 845	
aaa tct gtg act tcg gtc gtc tca acc ttg ttt tac gac aaa aaa atg	2592
Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met	
850 855 860	
aga acg acg aat ccg aaa gag act aag att gtg att gac act acc ggc	2640
Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly	
865 870 875 880	
agt acc aaa cct aag cag gac gat ctc att ctc act tgt ttc aga ggg	2688
Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly	
885 890 895	
tgg gtg aag cag ttg caa ata gat tac aaa ggc aac gaa ata atg acg	2736
Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr	
900 905 910	
gca gct gcc tct caa ggg ctg acc cgt aaa ggt gtg tat gcc gtt cgg	2784
Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg	
915 920 925	
tac aag gtg aat gaa aat cct ctg tac gca ccc acc tca gaa cat gtg	2832
Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val	
930 935 940	
aac gtc cta ctg acc cgc acg gag gac cgc atc gtg tgg aaa aca cta	2880
Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu	
945 950 955 960	
gcc ggc gac cca tgg ata aaa aca ctg act gcc aag tac cct ggg aat	2928
Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn	
965 970 975	
ttc act gcc acg ata gag gag tgg caa gca gag cat gat gcc atc atg	2976
Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met	
980 985 990	

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agg cac atc ttg gag aga ccg gac cct acc gac gtc ttc cag aat aag	3024
Arg His Ile Leu Glu Arg Pro Asp Pro Thr Asp Val Phe Gln Asn Lys	
995 1000 1005	
gca aac gtg tgt tgg gcc aag gct tta gtg ccg gtg ctg aag acc gct	3072
Ala Asn Val Cys Trp Ala Lys Ala Leu Val Pro Val Leu Lys Thr Ala	
1010 1015 1020	
ggc ata gac atg acc act gaa caa tgg aac act gtg gat tat ttt gaa	3120
Gly Ile Asp Met Thr Thr Glu Gln Trp Asn Thr Val Asp Tyr Phe Glu	
1025 1030 1035 1040	
acg gac aaa gct cac tca gca gag ata gta ttg aac caa cta tgc gtg	3168
Thr Asp Lys Ala His Ser Ala Glu Ile Val Leu Asn Gln Leu Cys Val	
1045 1050 1055	
agg ttc ttt gga ctc gat ctg gac tcc ggt cta ttt tct gca ccc act	3216
Arg Phe Phe Gly Leu Asp Leu Asp Ser Gly Leu Phe Ser Ala Pro Thr	
1060 1065 1070	
gtt ccg tta tcc att agg aat aat cac tgg gat aac tcc ccg tcg cct	3264
Val Pro Leu Ser Ile Arg Asn Asn His Trp Asp Asn Ser Pro Ser Pro	
1075 1080 1085	
aac atg tac ggg ctg aat aaa gaa gtg gtc cgt cag ctc tct cgc agg	3312
Asn Met Tyr Gly Leu Asn Lys Glu Val Val Arg Gln Leu Ser Arg Arg	
1090 1095 1100	
tac cca caa ctg cct cgg gca gtt gcc act gga aga gtc tat gac atg	3360
Tyr Pro Gln Leu Pro Arg Ala Val Ala Thr Gly Arg Val Tyr Asp Met	
1105 1110 1115 1120	
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Asn Thr Gly Thr Leu Arg Asn Tyr Asp Pro Arg Ile Asn Leu Val Pro	
1125 1130 1135	
gta aac aga aga ctg cct cat gct tta gtc ctc cac cat aat gaa cac	3456
Val Asn Arg Arg Leu Pro His Ala Leu Val Leu His His Asn Glu His	
1140 1145 1150	
cca cag agt gac ttt tct tca ttc gtc agc aaa ttg aag ggc aga act	3504
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1155 1160 1165	
gtc ctg gtg gtc ggg gaa aag ttg tcc gtc cca ggc aaa atg gtt gac	3552
Val Leu Val Val Gly Glu Lys Leu Ser Val Pro Gly Lys Met Val Asp	
1170 1175 1180	
tgg ttg tca gac cgg cct gag gct acc ttc aga gct cgg ctg gat tta	3600
Trp Leu Ser Asp Arg Pro Glu Ala Thr Phe Arg Ala Arg Leu Asp Leu	
1185 1190 1195 1200	
ggc atc cca ggt gat gtg ccc aaa tat gac ata ata ttt gtt aat gtg	3648
Gly Ile Pro Gly Asp Val Pro Lys Tyr Asp Ile Ile Phe Val Asn Val	
1205 1210 1215	

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agg acc cca tat aaa tac cat cac tat cag cag tgt gaa gac cat gcc	3696
Arg Thr Pro Tyr Lys Tyr His His Tyr Gln Gln Cys Glu Asp His Ala	
1220 1225 1230	
att aag ctt agc atg ttg acc aag aaa gct tgt ctg cat ctg aat ccc	3744
Ile Lys Leu Ser Met Leu Thr Lys Lys Ala Cys Leu His Leu Asn Pro	
1235 1240 1245	
ggc gga acc tgt gtc agc ata ggt tat ggt tac gct gac agg gcc agc	3792
Gly Gly Thr Cys Val Ser Ile Gly Tyr Gly Tyr Ala Asp Arg Ala Ser	
1250 1255 1260	
gaa agc atc att ggt gct ata gcg cgg cag ttc aag ttt tcc cgg gta	3840
Glu Ser Ile Ile Gly Ala Ile Ala Arg Gln Phe Lys Phe Ser Arg Val	
1265 1270 1275 1280	
tgc aaa ccg aaa tcc tca ctt gaa gag acg gaa gtt ctg ttt gta ttc	3888
Cys Lys Pro Lys Ser Ser Leu Glu Glu Thr Glu Val Leu Phe Val Phe	
1285 1290 1295	
att ggg tac gat cgc aag gcc cgt acg cac aat cct tac aag ctt tca	3936
Ile Gly Tyr Asp Arg Lys Ala Arg Thr His Asn Pro Tyr Lys Leu Ser	
1300 1305 1310	
tca acc ttg acc aac att tat aca ggt tcc aga ctc cac gaa gcc gga	3984
Ser Thr Leu Thr Asn Ile Tyr Thr Gly Ser Arg Leu His Glu Ala Gly	
1315 1320 1325	
tgt gca ccc tca tat cat gtg gtg cga ggg gat att gcc acg gcc acc	4032
Cys Ala Pro Ser Tyr His Val Val Arg Gly Asp Ile Ala Thr Ala Thr	
1330 1335 1340	
gaa gga gtg att ata aat gct gct aac agc aaa gga caa cct ggc gga	4080
Glu Gly Val Ile Ile Asn Ala Ala Asn Ser Lys Gly Gln Pro Gly Gly	
1345 1350 1355 1360	
ggg gtg tgc gga gcg ctg tat aag aag ttc ccg gaa agc ttc gat tta	4128
Gly Val Cys Gly Ala Leu Tyr Lys Lys Phe Pro Glu Ser Phe Asp Leu	
1365 1370 1375	
cag ccg atc gaa gta gga aaa gcg cga ctg gtc aaa ggt gca gct aaa	4176
Gln Pro Ile Glu Val Gly Lys Ala Arg Leu Val Lys Gly Ala Ala Lys	
1380 1385 1390	
cat atc att cat gcc gta gga cca aac ttc aac aaa gtt tcg gag gtt	4224
His Ile Ile His Ala Val Gly Pro Asn Phe Asn Lys Val Ser Glu Val	
1395 1400 1405	
gaa ggt gac aaa cag ttg gca gag gct tat gag tcc atc gct aag att	4272
Glu Gly Asp Lys Gln Leu Ala Glu Ala Tyr Glu Ser Ile Ala Lys Ile	
1410 1415 1420	
gtc aac gat aac aat tac aag tca gta gcg att cca ctg ttg tcc acc	4320
Val Asn Asp Asn Asn Tyr Lys Ser Val Ala Ile Pro Leu Leu Ser Thr	
1425 1430 1435 1440	

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ggc atc ttt tcc ggg aac aaa gat cga cta acc caa tca ttg aac cat 4368  
 Gly Ile Phe Ser Gly Asn Lys Asp Arg Leu Thr Gln Ser Leu Asn His  
 1445 1450 1455

ttg ctg aca gct tta gac acc act gat gca gat gta gcc ata tac tgc 4416  
 Leu Leu Thr Ala Leu Asp Thr Thr Asp Ala Asp Val Ala Ile Tyr Cys  
 1460 1465 1470

agg gac aag aaa tgg gaa atg act ctc aag gaa gca gtg gct agg aga 4464  
 Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg  
 1475 1480 1485

gaa gca gtg gag gag ata tgc ata tcc gac gac tct tca gtg aca gaa 4512  
 Glu Ala Val Glu Glu Ile Cys Ile Ser Asp Asp Ser Ser Val Thr Glu  
 1490 1495 1500

cct gat gca gag ctg gtg agg gtg cat ccg aag agt tct ttg gct gga 4560  
 Pro Asp Ala Glu Leu Val Arg Val His Pro Lys Ser Ser Leu Ala Gly  
 1505 1510 1515 1520

agg aag ggc tac agc aca agc gat ggc aaa act ttc tca tat ttg gaa 4608  
 Arg Lys Gly Tyr Ser Thr Ser Asp Gly Lys Thr Phe Ser Tyr Leu Glu  
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ggg acc aag ttt cac cag gcg gcc aag gat ata gca gaa att aat gcc 4656  
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 1540 1545 1550

atg tgg ccc gtt gca acg gag gcc aat gag cag gta tgc atg tat atc 4704  
 Met Trp Pro Val Ala Thr Glu Ala Asn Glu Gln Val Cys Met Tyr Ile  
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ctc gga gaa agc atg agc agt att agg tgc aaa tgc ccc gtc gaa gag 4752  
 Leu Gly Glu Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu  
 1570 1575 1580

tcg gaa gcc tcc aca cca cct agc acg ctg cct tgc ttg tgc atc cat 4800  
 Ser Glu Ala Ser Thr Pro Pro Ser Thr Leu Pro Cys Leu Cys Ile His  
 1585 1590 1595 1600

gcc atg act cca gaa aga gta cag cgc cta aaa gcc tca cgt cca gaa 4848  
 Ala Met Thr Pro Glu Arg Val Gln Arg Leu Lys Ala Ser Arg Pro Glu  
 1605 1610 1615

caa att act gtg tgc tca tcc ttt cca ttg ccg aag tat aga atc act 4896  
 Gln Ile Thr Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr Arg Ile Thr  
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ggg gtg cag aag atc caa tgc tcc cag cct ata ttg ttc tca ccg aaa 4944  
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 1635 1640 1645

gtg cct gcg tat att cat cca agg aag tat ctc gtg gaa aca cca ccg 4992  
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 1650 1655 1660

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Val Asp Glu Thr Pro Glu Pro Ser Ala Glu Asn Gln Ser Thr Glu Gly	
1665 1670 1675 1680	
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Thr Pro Glu Gln Pro Pro Leu Ile Thr Glu Asp Glu Thr Arg Thr Arg	
1685 1690 1695	
acg cct gag ccg atc atc atc gaa gag gaa gaa gag gat agc ata agt	5136
Thr Pro Glu Pro Ile Ile Ile Glu Glu Glu Glu Glu Asp Ser Ile Ser	
1700 1705 1710	
ttg ctg tca gat ggc ccg acc cac cag gtg ctg caa gtc gag gca gac	5184
Leu Leu Ser Asp Gly Pro Thr His Gln Val Leu Gln Val Glu Ala Asp	
1715 1720 1725	
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Ile His Gly Pro Pro Ser Val Ser Ser Ser Ser Trp Ser Ile Pro His	
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Ala Ser Asp Phe Asp Val Asp Ser Leu Ser Ile Leu Asp Thr Leu Glu	
1745 1750 1755 1760	
gga gct agc gtg acc agc ggg gca acg tca gcc gag act aac tct tac	5328
Gly Ala Ser Val Thr Ser Gly Ala Thr Ser Ala Glu Thr Asn Ser Tyr	
1765 1770 1775	
ttc gca aag agt atg gag ttt ctg gcg cga ccg gtg cct gcg cct cga	5376
Phe Ala Lys Ser Met Glu Phe Leu Ala Arg Pro Val Pro Ala Pro Arg	
1780 1785 1790	
aca gta ttc agg aac cct cca cat ccc gct ccg cgc aca aga aca ccg	5424
Thr Val Phe Arg Asn Pro Pro His Pro Ala Pro Arg Thr Arg Thr Pro	
1795 1800 1805	
tca ctt gca ccc agc agg gcc tgc tcc aga acc agc cta gtt tcc acc	5472
Ser Leu Ala Pro Ser Arg Ala Cys Ser Arg Thr Ser Leu Val Ser Thr	
1810 1815 1820	
ccg cca ggc gtg aat agg gtg atc act aga gag gag ctc gag gcg ctt	5520
Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Leu Glu Ala Leu	
1825 1830 1835 1840	
acc ccg tca cgc act cct agc agg tcc gtc tcc aga acc agc ctg gtc	5568
Thr Pro Ser Arg Thr Pro Ser Arg Ser Val Ser Arg Thr Ser Leu Val	
1845 1850 1855	
tcc aac ccg cca ggc gta aat agg gtg att aca aga gag gag ttt gag	5616
Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu	
1860 1865 1870	
gcg ttc gta gca caa caa caa tga cgg ttt gat gcg ggt gca tac atc	5664
Ala Phe Val Ala Gln Gln Gln * Arg Phe Asp Ala Gly Ala Tyr Ile	
1875 1880 1885	

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ttt tcc tcc gac acc ggt caa ggg cat tta caa caa aaa tca gta agg	5712
Phe Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg	
1890 1895 1900	
caa acg gtg cta tcc gaa gtg gtg ttg gag agg acc gaa ttg gag att	5760
Gln Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile	
1905 1910 1915	
tcg tat gcc ccg cgc ctc gac caa gaa aaa gaa gaa tta cta cgc aag	5808
Ser Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys	
1920 1925 1930 1935	
aaa tta cag tta aat ccc aca cct gct aac aga agc aga tac cag tcc	5856
Lys Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser	
1940 1945 1950	
agg aag gtg gag aac atg aaa gcc ata aca gct aga cgt att ctg caa	5904
Arg Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln	
1955 1960 1965	
ggc cta ggg cat tat ttg aag gca gaa gga aaa gtg gag tgc tac cga	5952
Gly Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg	
1970 1975 1980	
acc ctg cat cct gtt cct ttg tat tca tct agt gtg aac cgt gcc ttt	6000
Thr Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe	
1985 1990 1995	
tca agc ccc aag gtc gca gtg gaa gcc tgt aac gcc atg ttg aaa gag	6048
Ser Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu	
2000 2005 2010 2015	
aac ttt ccg act gtg gct tct tac tgt att att cca gag tac gat gcc	6096
Asn Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala	
2020 2025 2030	
tat ttg gac atg gtt gac gga gct tca tgc tgc tta gac act gcc agt	6144
Tyr Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser	
2035 2040 2045	
ttt tgc cct gca aag ctg cgc agc ttt cca aag aaa cac tcc tat ttg	6192
Phe Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu	
2050 2055 2060	
gaa ccc aca ata cga tcg gca gtg cct tca gcg atc cag aac acg ctc	6240
Glu Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu	
2065 2070 2075	
cag aac gtc ctg gca gct gcc aca aaa aga aat tgc aat gtc acg caa	6288
Gln Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln	
2080 2085 2090 2095	
atg aga gaa ttg ccc gta ttg gat tcg gcg gcc ttt aat gtg gaa tgc	6336
Met Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys	
2100 2105 2110	
ttc aag aaa tat gcg tgt aat aat gaa tat tgg gaa acg ttt aaa gaa	6384
Phe Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu	
2115 2120 2125	

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aac ccc atc agg ctt act gaa gaa aac gtg gta aat tac att acc aaa	6432
Asn Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys	
2130 2135 2140	
tta aaa gga cca aaa gct gct gct ctt ttt gcg aag aca cat aat ttg	6480
Leu Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu	
2145 2150 2155	
aat atg ttg cag gac ata cca atg gac agg ttt gta atg gac tta aag	6528
Asn Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys	
2160 2165 2170 2175	
aga gac gtg aaa gtg act cca gga aca aaa cat act gaa gaa cgg ccc	6576
Arg Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro	
2180 2185 2190	
aag gta cag gtg atc cag gct gcc gat ccg cta gca aca gcg tat ctg	6624
Lys Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu	
2195 2200 2205	
tgc gga atc cac cga gag ctg gtt agg aga tta aat gcg gtc ctg ctt	6672
Cys Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu	
2210 2215 2220	
ccg aac att cat aca ctg ttt gat atg tcg gct gaa gac ttt gac gct	6720
Pro Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala	
2225 2230 2235	
att ata gcc gag cac ttc cag cct ggg gat tgt gtt ctg gaa act gac	6768
Ile Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp	
2240 2245 2250 2255	
atc gcg tcg ttt gat aaa agt gag gac gac gcc atg gct ctg acc gcg	6816
Ile Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala	
2260 2265 2270	
tta atg att ctg gaa gac tta ggt gtg gac gca gag ctg ttg acg ctg	6864
Leu Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu	
2275 2280 2285	
att gag gcg gct ttc ggc gaa att tca tca ata cat ttg ccc act aaa	6912
Ile Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys	
2290 2295 2300	
act aaa ttt aaa ttc gga gcc atg atg aaa tct gga atg ttc ctc aca	6960
Thr Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr	
2305 2310 2315	
ctg ttt gtg aac aca gtc att aac att gta atc gca agc aga gtg ttg	7008
Leu Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu	
2320 2325 2330 2335	
aga gaa cgg cta acc gga tca cca tgt gca gca ttc att gga gat gac	7056
Arg Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp	
2340 2345 2350	
aat atc gtg aaa gga gtc aaa tcg gac aaa tta atg gca gac agg tgc	7104
Asn Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys	
2355 2360 2365	

0901258 111601

gcc acc tgg ttg aat atg gaa gtc aag att ata gat gct gtg gtg ggc 7152  
 Ala Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly  
           2370                          2375                          2380

gag aaa gcg ccc tat ttc tgt gga ggg ttt att ttg tgt gac tcc gtg 7200  
 Glu Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val  
           2385                          2390                          2395

acc ggc aca gcg tgc cgt gtg gca gac ccc cta aaa agg ctg ttt aag 7248  
 Thr Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys  
           2400                          2405                          2410                          2415

ctt ggc aaa cct ctg gca gca gac gat gaa cat gat gat gac agg aga 7296  
 Leu Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg  
                           2420                          2425                          2430

agg gca ttg cat gaa gag tca aca cgc tgg aac cga gtg ggt att ctt 7344  
 Arg Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu  
                           2435                          2440                          2445

tca gag ctg tgc aag gca gta gaa tca agg tat gaa acc gta gga act 7392  
 Ser Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr  
           2450                          2455                          2460

tcc atc ata gtt atg gcc atg act act cta gct agc agt gtt aaa tca 7440  
 Ser Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser  
           2465                          2470                          2475

ttc agc tac ctg aga ggg gcc cct ata act ctc tac ggc 7479  
 Phe Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly  
           2480                          2485                          2490

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 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 3

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   1                          5                          10                          15  
 Ala Leu Gln Arg Ser Phe Pro Gln Phe Glu Val Glu Ala Lys Gln Val  
           20                          25                          30  
 Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser  
           35                          40                          45  
 Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile  
           50                          55                          60  
 Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys  
   65                          70                          75                          80  
 Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr  
           85                          90                          95  
 Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu  
           100                          105                          110

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Asp	Lys	Lys	Met	Lys	Glu	Leu	Ala	Ala	Val	Met	Ser	Asp	Pro	Asp	Leu
		115					120					125			
Glu	Thr	Glu	Thr	Met	Cys	Leu	His	Asp	Asp	Glu	Ser	Cys	Arg	Tyr	Glu
	130					135					140				
Gly	Gln	Val	Ala	Val	Tyr	Gln	Asp	Val	Tyr	Ala	Val	Asp	Gly	Pro	Thr
					150					155					160
Ser	Leu	Tyr	His	Gln	Ala	Asn	Lys	Gly	Val	Arg	Val	Ala	Tyr	Trp	Ile
				165					170					175	
Gly	Phe	Asp	Thr	Thr	Pro	Phe	Met	Phe	Lys	Asn	Leu	Ala	Gly	Ala	Tyr
			180				185						190		
Pro	Ser	Tyr	Ser	Thr	Asn	Trp	Ala	Asp	Glu	Thr	Val	Leu	Thr	Ala	Arg
		195				200						205			
Asn	Ile	Gly	Leu	Cys	Ser	Ser	Asp	Val	Met	Glu	Arg	Ser	Arg	Arg	Gly
	210					215					220				
Met	Ser	Ile	Leu	Arg	Lys	Lys	Tyr	Leu	Lys	Pro	Ser	Asn	Asn	Val	Leu
	225				230					235					240
Phe	Ser	Val	Gly	Ser	Thr	Ile	Tyr	His	Glu	Lys	Arg	Asp	Leu	Leu	Arg
			245						250					255	
Ser	Trp	His	Leu	Pro	Ser	Val	Phe	His	Leu	Arg	Gly	Lys	Gln	Asn	Tyr
			260				265						270		
Thr	Cys	Arg	Cys	Glu	Thr	Ile	Val	Ser	Cys	Asp	Gly	Tyr	Val	Val	Lys
	275					280						285			
Arg	Ile	Ala	Ile	Ser	Pro	Gly	Leu	Tyr	Gly	Lys	Pro	Ser	Gly	Tyr	Ala
	290					295					300				
Ala	Thr	Met	His	Arg	Glu	Gly	Phe	Leu	Cys	Cys	Lys	Val	Thr	Asp	Thr
	305				310					315					320
Leu	Asn	Gly	Glu	Arg	Val	Ser	Phe	Pro	Val	Cys	Thr	Tyr	Val	Pro	Ala
			325						330					335	
Thr	Leu	Cys	Asp	Gln	Met	Thr	Gly	Ile	Leu	Ala	Thr	Asp	Val	Ser	Ala
			340				345						350		
Asp	Asp	Ala	Gln	Lys	Leu	Leu	Val	Gly	Leu	Asn	Gln	Arg	Ile	Val	Val
		355				360						365			
Asn	Gly	Arg	Thr	Gln	Arg	Asn	Thr	Asn	Thr	Met	Lys	Asn	Tyr	Leu	Leu
	370					375					380				
Pro	Val	Val	Ala	Gln	Ala	Phe	Ala	Arg	Trp	Ala	Lys	Glu	Tyr	Lys	Glu
	385				390					395					400
Asp	Gln	Glu	Asp	Glu	Arg	Pro	Leu	Gly	Leu	Arg	Asp	Arg	Gln	Leu	Val
			405					410						415	
<del>Met</del>	<del>Gly</del>	<del>Cys</del>	<del>Cys</del>	<del>Trp</del>	<del>Ala</del>	<del>Phe</del>	<del>Arg</del>	<del>Arg</del>	<del>His</del>	<del>Lys</del>	<del>Ile</del>	<del>Thr</del>	<del>Ser</del>	<del>Ile</del>	<del>Tyr</del>
			420					425					430		
Lys	Arg	Pro	Asp	Thr	Gln	Thr	Ile	Ile	Lys	Val	Asn	Ser	Asp	Phe	His
		435					440					445			
Ser	Phe	Val	Leu	Pro	Arg	Ile	Gly	Ser	Asn	Thr	Leu	Glu	Ile	Gly	Leu
	450					455					460				
Arg	Thr	Arg	Ile	Arg	Lys	Met	Leu	Glu	Glu	His	Lys	Glu	Pro	Ser	Pro
	465				470					475					480
Leu	Ile	Thr	Ala	Glu	Asp	Val	Gln	Glu	Ala	Lys	Cys	Ala	Ala	Asp	Glu
			485						490					495	
Ala	Lys	Glu	Val	Arg	Glu	Ala	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Pro	Pro
		500						505					510		
Leu	Ala	Ala	Asp	Val	Glu	Glu	Pro	Thr	Leu	Glu	Ala	Asp	Val	Asp	Leu
		515					520					525			
Met	Leu	Gln	Glu	Ala	Gly	Ala	Gly	Ser	Val	Glu	Thr	Pro	Arg	Gly	Leu
	530				535						540				
Ile	Lys	Val	Thr	Ser	Tyr	Ala	Gly	Glu	Asp	Lys	Ile	Gly	Ser	Tyr	Ala
	545				550					555					560

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Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile  
 565 570 575  
 His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys  
 580 585 590  
 Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu  
 595 600 605  
 Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala  
 610 615 620  
 Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His  
 625 630 635 640  
 Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys  
 645 650 655  
 Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp  
 660 665 670  
 Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr  
 675 680 685  
 Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu  
 690 695 700  
 Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr  
 705 710 715 720  
 Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr  
 725 730 735  
 Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile  
 740 745 750  
 Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr  
 755 760 765  
 Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu  
 770 775 780  
 Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu  
 785 790 795 800  
 Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys  
 805 810 815  
 Gln Cys Gly Phe Asn Met Met Cys Leu Lys Val His Phe Asn His  
 820 825 830  
  
 Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr  
 835 840 845  
 Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met  
 850 855 860  


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 Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly  
 865 870 875 880  
 Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly  
 885 890 895  
 Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr  
 900 905 910  
 Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg  
 915 920 925  
 Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val  
 930 935 940  
 Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu  
 945 950 955 960  
 Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn  
 965 970 975  
 Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met  
 980 985 990

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Arg His Ile Leu Glu Arg Pro Asp Pro Thr Asp Val Phe Gln Asn Lys  
 995 1000 1005  
 Ala Asn Val Cys Trp Ala Lys Ala Leu Val Pro Val Leu Lys Thr Ala  
 1010 1015 1020  
 Gly Ile Asp Met Thr Thr Glu Gln Trp Asn Thr Val Asp Tyr Phe Glu  
 1025 1030 1035 1040  
 Thr Asp Lys Ala His Ser Ala Glu Ile Val Leu Asn Gln Leu Cys Val  
 1045 1050 1055  
 Arg Phe Phe Gly Leu Asp Leu Asp Ser Gly Leu Phe Ser Ala Pro Thr  
 1060 1065 1070  
 Val Pro Leu Ser Ile Arg Asn Asn His Trp Asp Asn Ser Pro Ser Pro  
 1075 1080 1085  
 Asn Met Tyr Gly Leu Asn Lys Glu Val Val Arg Gln Leu Ser Arg Arg  
 1090 1095 1100  
 Tyr Pro Gln Leu Pro Arg Ala Val Ala Thr Gly Arg Val Tyr Asp Met  
 1105 1110 1115 1120  
 Asn Thr Gly Thr Leu Arg Asn Tyr Asp Pro Arg Ile Asn Leu Val Pro  
 1125 1130 1135  
 Val Asn Arg Arg Leu Pro His Ala Leu Val Leu His His Asn Glu His  
 1140 1145 1150  
 Pro Gln Ser Asp Phe Ser Ser Phe Val Ser Lys Leu Lys Gly Arg Thr  
 1155 1160 1165  
 Val Leu Val Val Gly Glu Lys Leu Ser Val Pro Gly Lys Met Val Asp  
 1170 1175 1180  
 Trp Leu Ser Asp Arg Pro Glu Ala Thr Phe Arg Ala Arg Leu Asp Leu  
 1185 1190 1195 1200  
 Gly Ile Pro Gly Asp Val Pro Lys Tyr Asp Ile Ile Phe Val Asn Val  
 1205 1210 1215  
 Arg Thr Pro Tyr Lys Tyr His His Tyr Gln Gln Cys Glu Asp His Ala  
 1220 1225 1230  
 Ile Lys Leu Ser Met Leu Thr Lys Lys Ala Cys Leu His Leu Asn Pro  
 1235 1240 1245  
 Gly Gly Thr Cys Val Ser Ile Gly Tyr Gly Tyr Ala Asp Arg Ala Ser  
 1250 1255 1260  
  
 Glu Ser Ile Ile Gly Ala Ile Ala Arg Gln Phe Lys Phe Ser Arg Val  
 1265 1270 1275 1280  
 Cys Lys Pro Lys Ser Ser Leu Glu Glu Thr Glu Val Leu Phe Val Phe  
 1285 1290 1295  


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 Ile Gly Tyr Asp Arg Lys Ala Arg Thr His Asn Pro Tyr Lys Leu Ser  
 1300 1305 1310  
 Ser Thr Leu Thr Asn Ile Tyr Thr Gly Ser Arg Leu His Glu Ala Gly  
 1315 1320 1325  
 Cys Ala Pro Ser Tyr His Val Val Arg Gly Asp Ile Ala Thr Ala Thr  
 1330 1335 1340  
 Glu Gly Val Ile Ile Asn Ala Ala Asn Ser Lys Gly Gln Pro Gly Gly  
 1345 1350 1355 1360  
 Gly Val Cys Gly Ala Leu Tyr Lys Lys Phe Pro Glu Ser Phe Asp Leu  
 1365 1370 1375  
 Gln Pro Ile Glu Val Gly Lys Ala Arg Leu Val Lys Gly Ala Ala Lys  
 1380 1385 1390  
 His Ile Ile His Ala Val Gly Pro Asn Phe Asn Lys Val Ser Glu Val  
 1395 1400 1405  
  
 Glu Gly Asp Lys Gln Leu Ala Glu Ala Tyr Glu Ser Ile Ala Lys Ile  
 1410 1415 1420

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Val Asn Asp Asn Asn Tyr Lys Ser Val Ala Ile Pro Leu Leu Ser Thr  
 1425 1430 1435 1440  
 Gly Ile Phe Ser Gly Asn Lys Asp Arg Leu Thr Gln Ser Leu Asn His  
 1445 1450 1455  
 Leu Leu Thr Ala Leu Asp Thr Thr Asp Ala Asp Val Ala Ile Tyr Cys  
 1460 1465 1470  
 Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg  
 1475 1480 1485  
 Glu Ala Val Glu Glu Ile Cys Ile Ser Asp Asp Ser Ser Val Thr Glu  
 1490 1495 1500  
 Pro Asp Ala Glu Leu Val Arg Val His Pro Lys Ser Ser Leu Ala Gly  
 1505 1510 1515 1520  
 Arg Lys Gly Tyr Ser Thr Ser Asp Gly Lys Thr Phe Ser Tyr Leu Glu  
 1525 1530 1535  
 Gly Thr Lys Phe His Gln Ala Ala Lys Asp Ile Ala Glu Ile Asn Ala  
 1540 1545 1550  
 Met Trp Pro Val Ala Thr Glu Ala Asn Glu Gln Val Cys Met Tyr Ile  
 1555 1560 1565  
 Leu Gly Glu Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu  
 1570 1575 1580  
 Ser Glu Ala Ser Thr Pro Pro Ser Thr Leu Pro Cys Leu Cys Ile His  
 1585 1590 1595 1600  
 Ala Met Thr Pro Glu Arg Val Gln Arg Leu Lys Ala Ser Arg Pro Glu  
 1605 1610 1615  
 Gln Ile Thr Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr Arg Ile Thr  
 1620 1625 1630  
 Gly Val Gln Lys Ile Gln Cys Ser Gln Pro Ile Leu Phe Ser Pro Lys  
 1635 1640 1645  
 Val Pro Ala Tyr Ile His Pro Arg Lys Tyr Leu Val Glu Thr Pro Pro  
 1650 1655 1660  
 Val Asp Glu Thr Pro Glu Pro Ser Ala Glu Asn Gln Ser Thr Glu Gly  
 1665 1670 1675 1680  
 Thr Pro Glu Gln Pro Pro Leu Ile Thr Glu Asp Glu Thr Arg Thr Arg  
 1685 1690 1695  
  
 Thr Pro Glu Pro Ile Ile Ile Glu Glu Glu Glu Glu Asp Ser Ile Ser  
 1700 1705 1710  
 Leu Leu Ser Asp Gly Pro Thr His Gln Val Leu Gln Val Glu Ala Asp  
 1715 1720 1725  
~~Ile His Gly Pro Pro Ser Val Ser Ser Ser Ser Trp Ser Ile Pro His~~  
~~1730 1735 1740~~  
 Ala Ser Asp Phe Asp Val Asp Ser Leu Ser Ile Leu Asp Thr Leu Glu  
 1745 1750 1755 1760  
 Gly Ala Ser Val Thr Ser Gly Ala Thr Ser Ala Glu Thr Asn Ser Tyr  
 1765 1770 1775  
 Phe Ala Lys Ser Met Glu Phe Leu Ala Arg Pro Val Pro Ala Pro Arg  
 1780 1785 1790  
 Thr Val Phe Arg Asn Pro Pro His Pro Ala Pro Arg Thr Arg Thr Pro  
 1795 1800 1805  
 Ser Leu Ala Pro Ser Arg Ala Cys Ser Arg Thr Ser Leu Val Ser Thr  
 1810 1815 1820  
  
 Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Leu Glu Ala Leu  
 1825 1830 1835 1840  
 Thr Pro Ser Arg Thr Pro Ser Arg Ser Val Ser Arg Thr Ser Leu Val  
 1845 1850 1855

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Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu  
 1860 1865 1870  
 Ala Phe Val Ala Gln Gln Gln Arg Phe Asp Ala Gly Ala Tyr Ile Phe  
 1875 1880 1885  
 Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg Gln  
 1890 1895 1900  
 Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile Ser  
 1905 1910 1915 1920  
 Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys Lys  
 1925 1930 1935  
 Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser Arg  
 1940 1945 1950  
 Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln Gly  
 1955 1960 1965  
 Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg Thr  
 1970 1975 1980  
 Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe Ser  
 1985 1990 1995 2000  
 Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu Asn  
 2005 2010 2015  
 Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala Tyr  
 2020 2025 2030  
 Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser Phe  
 2035 2040 2045  
 Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu Glu  
 2050 2055 2060  
 Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu Gln  
 2065 2070 2075 2080  
 Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln Met  
 2085 2090 2095  
 Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys Phe  
 2100 2105 2110  
 Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu Asn  
 2115 2120 2125  
  
 Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys Leu  
 2130 2135 2140  
 Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Asn  
 2145 2150 2155 2160  
~~Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys Arg~~  
~~2165 2170 2175~~  
 Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro Lys  
 2180 2185 2190  
 Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu Cys  
 2195 2200 2205  
 Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu Pro  
 2210 2215 2220  
 Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile  
 2225 2230 2235 2240  
  
 Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp Ile  
 2245 2250 2255  
 Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala Leu  
 2260 2265 2270  
 Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu Ile  
 2275 2280 2285

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Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys Thr  
 2290 2295 2300  
 Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu  
 2305 2310 2315 2320  
 Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu Arg  
 2325 2330 2335  
 Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp Asn  
 2340 2345 2350  
 Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys Ala  
 2355 2360 2365  
 Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly Glu  
 2370 2375 2380  
 Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val Thr  
 2385 2390 2395 2400  
 Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu  
 2405 2410 2415  
 Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg Arg  
 2420 2425 2430  
 Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu Ser  
 2435 2440 2445  
 Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr Ser  
 2450 2455 2460  
 Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser Phe  
 2465 2470 2475 2480  
 Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly  
 2485 2490

&lt;210&gt; 4

&lt;211&gt; 1476

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(1476)

&lt;400&gt; 4

atg gct gcg aga gcg tca ata tta aga ggg gaa aaa tta gat aaa tgg	48
Met Ala Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp	
1 5 10 15	
 gaa aag att agg tta agg cca ggg gga aag aaa cat tat atg tta aaa	96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys	
20 25 30	
 cac ata gta tgg gcg agc agg gag ctg gaa aga ttt gca ctt aac cct	144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro	
35 40 45	
 ggc ctt tta gaa aca tca gaa gga tgt aaa caa ata atg aaa cag cta	192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu	
50 55 60	

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caa cca gct ctc cag aca gga aca gag gaa ctt aaa tca tta tac aac	240
Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn	
65 70 75 80	
aca gta gca act ctc tat tgt gta cat gaa aag ata gaa gta cga gac	288
Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp	
85 90 95	
acc aag gaa gcc tta gat aag ata gag gaa gaa caa aac aaa tgt cag	336
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln	
100 105 110	
caa aaa acg cag cag gca aaa gcg gct gac ggg aaa gtc agt caa aat	384
Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn	
115 120 125	
tat cct ata gtg cag aat ctc caa ggg caa atg gta cat caa gcc ata	432
Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile	
130 135 140	
tca cct aga acc ttg aat gca tgg gta aaa gta ata gaa gaa aag gct	480
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala	
145 150 155 160	
ttt agc cca gag gta ata ccc atg ttt aca gca tta tca gaa gga gcc	528
Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala	
165 170 175	
acc cca caa gat tta aac acc atg tta aat aca gtg ggg gga cac caa	576
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
180 185 190	
gca gcc atg caa atg tta aaa gat act att aat gaa gag gct gca gaa	624
Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu	
195 200 205	
tgg gat aga tta cat cca gtc cat gcg ggg cct att gca cca ggc cag	672
Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln	
210 215 220	
atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt	720
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu	
225 230 235 240	
cag gaa caa ata gca tgg atg aca agt aac cca cct att cca gtg gga	768
Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly	
245 250 255	
gac atc tat aaa aga tgg ata att ctg ggg tta aat aaa ata gtg aga	816
Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg	
260 265 270	
atg tat agc ccg gtc agc att ttg gac ata aga caa ggg cca aag gaa	864
Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu	
275 280 285	

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ccc ttt cga gac tat gta gat cgg ttc ttt aaa act tta aga gct gaa 912  
Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu  
290 295 300

caa gct aca caa gaa gta aaa aat tgg atg aca gac acc ttg tta gtc 960  
Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val  
305 310 315 320

caa aat gcg aac cca gat tgt aag acc att ttg aga gca tta gga cca 1008  
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro  
325 330 335

ggg gct aca tta gaa gaa atg atg aca gca tgt caa ggg gtg gga gga 1056  
Gly Ala Thr Leu Glu Glu Met Met Thr Thr Ala Cys Gln Gly Val Gly Gly  
340 345 350

cct ggc cac aaa gca aga gta ttg gct gag gca atg agt caa aca aac 1104  
Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn  
355 360 365

agt gga aac ata atg atg cag aga agc aat ttt aaa ggc cct aga aga 1152  
Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg  
370 375 380

att gtt aaa tgt ttt aac tgt ggc aag gaa ggg cac ata gcc aga aat 1200  
Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn  
385 390 395 400

tgc aga gcc cct agg aaa aaa ggc tgt tgg aaa tgt gga aaa gaa gga 1248  
Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly  
405 410 415

cac caa atg aaa gac tgc act gag agg cag gct aat ttt tta ggg aaa 1296  
His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys  
420 425 430

att tgg cct tcc cac aag ggg agg cca ggg aat ttc ctt cag aac aga 1344  
Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg  
435 440 445

cca gag cca aca gcc cca cca gca gag agc ttc agg ttc gaa gag aca 1392  
Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr  
450 455 460

acc ccc gct ccg aaa cag gag ccg ata gaa agg gaa ccc tta act tcc 1440  
Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser  
465 470 475 480

ctc aaa tca ctc ttt ggc agc gac ccc ttg tct caa 1476  
Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln  
485 490

<210> 5

<211> 492

<212> PRT

<213> Artificial Sequence

0001253.11601



&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 5

Met	Ala	Ala	Arg	Ala	Ser	Ile	Leu	Arg	Gly	Glu	Lys	Leu	Asp	Lys	Trp
1				5					10					15	
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	His	Tyr	Met	Leu	Lys
			20					25					30		
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Leu	Asn	Pro
		35					40					45			
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Lys	Gln	Ile	Met	Lys	Gln	Leu
	50					55					60				
Gln	Pro	Ala	Leu	Gln	Thr	Gly	Thr	Glu	Glu	Leu	Lys	Ser	Leu	Tyr	Asn
65					70					75					80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Glu	Lys	Ile	Glu	Val	Arg	Asp
			85					90						95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Cys	Gln
			100					105					110		
Gln	Lys	Thr	Gln	Gln	Ala	Lys	Ala	Ala	Asp	Gly	Lys	Val	Ser	Gln	Asn
		115					120					125			
Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile
	130					135					140				
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Ile	Glu	Glu	Lys	Ala
145					150					155					160
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Thr	Ala	Leu	Ser	Glu	Gly	Ala
			165					170						175	
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln
			180					185					190		
Ala	Ala	Met	Gln	Met	Leu	Lys	Asp	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu
		195					200					205			
Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln
	210					215					220				
Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu
225					230					235					240
Gln	Glu	Gln	Ile	Ala	Trp	Met	Thr	Ser	Asn	Pro	Pro	Ile	Pro	Val	Gly
			245						250					255	
Asp	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg
			260					265				270			
Met	Tyr	Ser	Pro	Val	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu
	275						280					285			
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Phe	Lys	Thr	Leu	Arg	Ala	Glu
	290					295					300				
Gln	Ala	Thr	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Asp	Thr	Leu	Leu	Val
305					310					315					320
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Arg	Ala	Leu	Gly	Pro
			325					330					335		
Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
		340						345				350			
Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	Gln	Thr	Asn
	355						360					365			
Ser	Gly	Asn	Ile	Met	Met	Gln	Arg	Ser	Asn	Phe	Lys	Gly	Pro	Arg	Arg
	370					375					380				
Ile	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	Ile	Ala	Arg	Asn
385					390					395					400

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Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly  
 405 410 415  
 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys  
 420 425 430  
 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg  
 435 440 445  
 Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr  
 450 455 460  
 Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser  
 465 470 475 480  
 Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln  
 485 490

&lt;210&gt; 6

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
 synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(813)

&lt;400&gt; 6

atg agc cat att caa cgg gaa acg tct tgc tgc agg ccg cga tta aat 48  
 Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn  
 1 5 10 15

tcc aac atg gat gct gat tta tat ggg tat aaa tgg gct cgc gat aat 96  
 Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn  
 20 25 30

gtc ggg caa tca ggt gcg aca atc tat cga ttg tat ggg aag ccc gat 144  
 Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp  
 35 40 45

gcg cca gag ttg ttt ctg aaa cat ggc aaa ggt agc gtt gcc aat gat 192  
 Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp  
 50 55 60

gtt aca gat gag atg gtc aga cta aac tgg ctg acg gaa ttt atg cct 240  
 Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro  
 65 70 75 80

ctt ccg acc atc aag cat ttt atc cgt act cct gat gat gca tgg tta 288  
 Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu  
 85 90 95

ctc acc act gcg atc ccc ggg aaa aca gca ttc cag gta tta gaa gaa 336  
 Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu  
 100 105 110

0991250.11601  
 T09T01"052T6660

tat cct gat tca ggt gaa aat att gtt gat gcg ctg gca gtg ttc ctg	384
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu	
115 120 125	
cgc cgg ttg cat tcg att cct gtt tgt aat tgt cct ttt aac agc gat	432
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp	
130 135 140	
cgc gta ttt cgt ctc gct cag gcg caa tca cga atg aat aac ggt ttg	480
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu	
145 150 155 160	
gtt gat gcg agt gat ttt gat gac gag cgt aat ggc tgg cct gtt gaa	528
Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu	
165 170 175	
caa gtc tgg aaa gaa atg cat aag ctt ttg cca ttc tca ccg gat tca	576
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser	
180 185 190	
gtc gtc act cat ggt gat ttc tca ctt gat aac ctt att ttt gac gag	624
Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu	
195 200 205	
ggg aaa tta ata ggt tgt att gat gtt gga cga gtc gga atc gca gac	672
Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp	
210 215 220	
cga tac cag gat ctt gcc atc cta tgg aac tgc ctc ggt gag ttt tct	720
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser	
225 230 235 240	
cct tca tta cag aaa cgg ctt ttt caa aaa tat ggt att gat aat cct	768
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro	
245 250 255	
gat atg aat aaa ttg cag ttt cat ttg atg ctc gat gag ttt ttc	813
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe	
260 265 270	

<210> 7  
 <211> 271  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 7  
 Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn  
 1 5 10 15  
 Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn  
 20 25 30

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Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp  
 35 40 45  
 Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp  
 50 55 60  
 Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro  
 65 70 75 80  
 Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu  
 85 90 95  
 Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu  
 100 105 110  
 Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu  
 115 120 125  
 Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp  
 130 135 140  
 Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu  
 145 150 155 160  
 Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu  
 165 170 175  
 Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser  
 180 185 190  
 Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu  
 195 200 205  
 Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp  
 210 215 220  
 Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser  
 225 230 235 240  
 Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro  
 245 250 255  
 Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe  
 260 265 270

&lt;210&gt; 8

&lt;211&gt; 5076

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
 synthetic construct

&lt;400&gt; 8

ataggcggcg	catgagagaa	gccagacca	attacctacc	caaaatggag	aaagtgcacg	60
ttgacatcga	ggaagacagc	ccattcctca	gagctttgca	gcggagcttc	ccgcagtttg	120
aggtagaagc	caagcaggtc	actgataatg	accatgctaa	tgccagagcg	ttttcgcatc	180
tggcttcaaa	actgatcgaa	acggaggtgg	acccatccga	cacgatcctt	gacattggaa	240
gtgcgcccgc	ccgcagaatg	tattctaagc	acaagtatca	ttgtatctgt	ccgatgagat	300
gtgcggaaga	tccggacaga	ttgtataagt	atgcaactaa	gctgaagaaa	aactgtaagg	360
aaataactga	taaggaattg	gacaagaaaa	tgaaggagct	cgccgccgtc	atgagcgacc	420
ctgacctgga	aactgagact	atgtgcctcc	acgacgacga	gtcgtgtcgc	tacgaagggc	480
aagtgcgtgt	ttaccaggat	gtatacgcg	ttgacggacc	ctataactct	ctacggctaa	540
cctgaatgga	ctacgacata	gtctagtccg	ccaagatggt	cccgttccag	ccaatgtatc	600
cgatgcagcc	aatgccctat	cgcaaccctg	tcgcggcccc	gcgcaggccc	tggttcccc	660
gaaccgaccc	ttttctggcg	atgcaggtgc	aggaattaac	ccgctcgatg	gctaacctga	720
cgttcaagca	acgccgggac	gcgccacctg	aggggccatc	cgctaagaaa	ccgaagaagg	780
aggcctcgca	aaaacagaaa	gggggaggcc	aagggaagaa	gaagaagaac	caagggaaga	840
agaaggctaa	gacagggccg	cctaataccga	aggcacagaa	tggaacaag	aagaagacca	900
acaagaaacc	aggcaagaga	cagcgcatgg	tcatgaaatt	ggaatctgac	aagacgttcc	960

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caatcatggt	ggaaggggaag	ataaacgggt	acgcttgtgt	ggtcggaggg	aagttattca	1020
ggccgatgca	tgtggaaggc	aagatcgaca	acgacgttct	ggccgcgctt	aagacgaaga	1080
aagcatccaa	atacgatctt	gagtatgcag	atgtgccaca	gaacatgcgg	gccgatacat	1140
tcaaatacac	ccatgagaaa	ccccagggt	attacagctg	gcacatgga	gcagtccaat	1200
atgaaaatgg	gcgtttcacg	gtgccgaaag	gagttggggc	caagggagac	agcggacgac	1260
ccattctgga	taaccaggga	cgggtggtcg	ctattgtgct	gggaggtgtg	aatgaaggat	1320
ctaggacagc	cctttcagtc	gtcatgtgga	acgagaaggg	agttaccgtg	aagtatactc	1380
cggagaactg	cgagcaatgg	tcactagtga	ccaccatgtg	tctgctcgcc	aatgtgacgt	1440
tcccatgtgc	tcaaccacca	atttgctacg	acagaaaacc	agcagagact	ttggccatgc	1500
tcagcgtaa	catccctgct	gggaggatca	gccgtaatta	ttataattgg	cttgggtgctg	1560
gctactattg	tggccatgta	cgtgctgacc	aaccagaaac	ataattgaat	acagcagcaa	1620
ttggcaagct	gottacatag	aactcgcggc	gattggcatg	ccgctttaaa	atTTTTattt	1680
tatttttctt	ttcttttccg	aatcggattt	tgtttttaat	atttcaaaaa	aaaaaaaaaa	1740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	gggaagagcg	cggccgcgcg	ctgggtctacg	1800
tcttgctggc	gttcgcgacg	cgaggctgga	tggccttccc	cattatgatt	cttctcgctt	1860
ccggcggcat	cggttgcccc	gcgttgacgg	ccatgctgtc	caggcaggta	gatgacgacc	1920
atcagggaca	gcttcaagga	tcgctcgccg	ctcttaccag	cctaacttcg	atcactggac	1980
cgctgatcgt	cacggcgatt	tatgccgcct	cggcgagcac	atggaacggg	ttggcatgga	2040
ttgtaggcgc	cgccctatac	cttgtctgcc	tccccgcggt	gcgtcgcggt	gcattggagcc	2100
gggccacctc	gacctgaatg	gaagccggcg	gcacctcgct	aacggattca	ccactccaag	2160
aattggagcc	aatcaattct	tgcggagaac	tgtgaatgcg	caaaccaacc	cttggcgagaa	2220
catatccatc	gcgtccgcca	tctccagcag	ccgcacgcgg	cgcactctcg	gcagcgtttg	2280
gtcctggcca	cgggtgcgca	tgatcgtgct	cctgtcgttg	aggacccggc	taggctggcg	2340
gggttgccct	actggttagc	agaatgaatc	accgatacgc	gagcgaacgt	gaagcgactg	2400
ctgctgcaaa	acgtctgcga	cctgagcaac	aacatgaatg	gtcttcgggt	tccgtgtttc	2460
gtaaagtctg	gaaacgcgga	agtcagcgcc	ctgcaccatt	atgttcggga	tctgcatcgc	2520
aggatgctgc	tggctaccct	gtggaacacc	tacatctgta	ttaacgaagc	gctggcattg	2580
accctgagtg	atTTTTctct	ggtcccgcgc	catccatacc	gccagttggt	tacctcaca	2640
acgttccagt	aaccgggcat	gttcatcatc	agtaaccctg	atcgtgagca	tctctctctg	2700
tttcatcggt	atcattaccc	ccatgaacag	aaatccccct	tacacggagg	catcagtgac	2760
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&lt;210&gt; 9

&lt;211&gt; 1026

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(1026)

&lt;400&gt; 9

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Met	Phe	Pro	Phe	Gln	Pro	Met	Tyr	Pro	Met	Gln	Pro	Met	Pro	Tyr	Arg	
1				5				10						15		

aac	ccg	ttc	gcg	gcc	ccg	cgc	agg	ccc	tgg	ttc	ccc	aga	acc	gac	cct	96
Asn	Pro	Phe	Ala	Ala	Pro	Arg	Arg	Pro	Trp	Phe	Pro	Arg	Thr	Asp	Pro	
			20					25					30			

ttt	ctg	gcg	atg	cag	gtg	cag	gaa	tta	acc	cgc	tcg	atg	gct	aac	ctg	144
Phe	Leu	Ala	Met	Gln	Val	Gln	Glu	Leu	Thr	Arg	Ser	Met	Ala	Asn	Leu	
			35				40					45				

acg	ttc	aag	caa	cgc	cgg	gac	gcg	cca	cct	gag	ggg	cca	tcc	gct	aag	192
Thr	Phe	Lys	Gln	Arg	Arg	Asp	Ala	Pro	Pro	Glu	Gly	Pro	Ser	Ala	Lys	
		50				55					60					

aaa	ccg	aag	aag	gag	gcc	tcg	caa	aaa	cag	aaa	ggg	gga	ggc	caa	ggg	240
Lys	Pro	Lys	Lys	Glu	Ala	Ser	Gln	Lys	Gln	Lys	Gly	Gly	Gly	Gln	Gly	
		65			70				75					80		

aag	aag	aag	aag	aac	caa	ggg	aag	aag	aag	gct	aag	aca	ggg	ccg	cct	288
Lys	Lys	Lys	Lys	Asn	Gln	Gly	Lys	Lys	Lys	Ala	Lys	Thr	Gly	Pro	Pro	
				85					90					95		

00991258.1.1601

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Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro	
100 105 110	
ggc aag aga cag cgc atg gtc atg aaa ttg gaa tct gac aag acg ttc	384
Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe	
115 120 125	
cca atc atg ttg gaa ggg aag ata aac ggc tac gct tgt gtg gtc gga	432
Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly	
130 135 140	
ggg aag tta ttc agg ccg atg cat gtg gaa ggc aag atc gac aac gac	480
Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp	
145 150 155 160	
gtt ctg gcc gcg ctt aag acg aag aaa gca tcc aaa tac gat ctt gag	528
Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu	
165 170 175	
tat gca gat gtg cca cag aac atg cgg gcc gat aca ttc aaa tac acc	576
Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr	
180 185 190	
cat gag aaa ccc caa ggc tat tac agc tgg cat cat gga gca gtc caa	624
His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln	
195 200 205	
tat gaa aat ggg cgt ttc acg gtg ccg aaa gga gtt ggg gcc aag gga	672
Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly	
210 215 220	
gac agc gga cga ccc att ctg gat aac cag gga cgg gtg gtc gct att	720
Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile	
225 230 235 240	
gtg ctg gga ggt gtg aat gaa gga tct agg aca gcc ctt tca gtc gtc	768
Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val	
245 250 255	
atg tgg aac gag aag gga gtt acc gtg aag tat act ccg gag aac tgc	816
Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys	
260 265 270	
gag caa tgg tca cta gtg acc acc atg tgt ctg ctc gcc aat gtg acg	864
Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr	
275 280 285	
ttc cca tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag	912
Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu	
290 295 300	
act ttg gcc atg ctc agc gtt aac atc cct gct ggg agg atc agc cgt	960
Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg	
305 310 315 320	

0991250-11601

aat tat tat aat tgg ctt ggt gct ggc tac tat tgt ggc cat gta cgt 1008  
 Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg  
                   325                  330                  335

gct gac caa cca gaa aca 1026  
 Ala Asp Gln Pro Glu Thr  
                   340

<210> 10  
 <211> 342  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
       synthetic construct

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 Asn Pro Phe Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro  
           20                  25                  30  
 Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu  
           35                  40                  45  
  
 Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys  
   50                  55                  60  
 Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly  
   65                  70                  75                  80  
  
 Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro  
           85                  90                  95  
 Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro  
          100                 105                 110  
 Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe  
          115                 120                 125  
 Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly  
          130                 135                 140  


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 Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp  
  145                 150                 155                 160  
 Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu  
          165                 170                 175  
 Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr  
          180                 185                 190  
 His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln  
          195                 200                 205  
 Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly  
          210                 215                 220  
 Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile  
  225                 230                 235                 240  
 Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val  
          245                 250                 255  
 Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys  
          260                 265                 270  
 Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr  
          275                 280                 285

09901258-11601



Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu  
 290 295 300  
 Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg  
 305 310 315 320  
 Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg  
 325 330 335  
 Ala Asp Gln Pro Glu Thr  
 340

&lt;210&gt; 11

&lt;211&gt; 6989

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 11

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agccactggt	aacaggatta	gcagagcgag	gtatgtaggc	ggtgctacag	agttcttgaa	5700

09991258 "11601"

gtgggtggcct aactacggct acactagaag gacagtatatt ggtatctgcg ctctgctgaa 5760  
gccagttacc ttcggaaaaa gagttggtag ctcttgatcc ggcaaaaaa ccaccgctgg 5820  
tagcgggtgg ttttttgttt gcaagcagca gattacgcgc agaaaaaaag gatctcaaga 5880  
agatcctttg atcttttcta cgggggtctga cgctcagtg aacgaaaact cacgttaagg 5940  
gattttgggtc atgaacaata aaactgtctg cttacataaa cagtaataca aggggtgtta 6000  
tgagccatat tcaacgggaa acgtcttgct cgaggccgcg attaaattcc aacatggatg 6060  
ctgatttata tgggtataaa tgggctcgcg ataatgtcgg gcaatcaggt gcgacaatct 6120  
atcgattgta tgggaagccc gatgcgccag agttgtttct gaaacatggc aaaggtagcg 6180  
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&lt;210&gt; 12

&lt;211&gt; 2943

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(2943)

&lt;400&gt; 12

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Met-Ser-Leu-Val-Thr-Thr-Met-Cys-Leu-Leu-Ala-Asn-Val-Thr-Phe-Pro

1

5

10

15

tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag act ttg 96

Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu

20

25

30

gcc atg ctc agc gtt aac gtt gac aac ccg ggc tac gat gag ctg ctg 144

Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu

35

40

45

gaa gca gct gtt aag tgc ccc gga agg aaa agg aga tcc acc gag gag 192

Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu

50

55

60

ctg ttt aag gag tat aag cta acg cgc cct tac atg gcc aga tgc atc 240

Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile

65

70

75

80

0991258.11601

aga tgt gca gtt ggg agc tgc cat agt cca ata gca atc gag gca gta	288
Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val	
85 90 95	
aag agc gac ggg cac gac ggt tat gtt aga ctt cag act tcc tcg cag	336
Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln	
100 105 110	
tat ggc ctg gat tcc tcc ggc aac tta aag ggc agg acc atg cgg tat	384
Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr	
115 120 125	
gac atg cac ggg acc att aaa gag ata cca cta cat caa gtg tca ctc	432
Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu	
130 135 140	
cat aca tct cgc ccg tgt cac att gtg gat ggg cac ggt tat ttc ctg	480
His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu	
145 150 155 160	
ctt gcc agg tgc ccg gca ggg gac tcc atc acc atg gaa ttt aag aaa	528
Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys	
165 170 175	
gat tcc gtc aca cac tcc tgc tcg gtg ccg tat gaa gtg aaa ttt aat	576
Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn	
180 185 190	
cct gta ggc aga gaa ctc tat act cat ccc cca gaa cac gga gta gag	624
Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu	
195 200 205	
caa gcg tgc caa gtc tac gca cat gat gca cag aac aga gga gct tat	672
Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr	
210 215 220	
gtc gag atg cac ctc cca ggc tca gaa gtg gac agc agt ttg gtt tcc	720
Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser	
225 230 235 240	
ttg agc ggc agt tca gtc acc gtg aca cct cct gtt ggg act agc gcc	768
Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala	
245 250 255	
ctg gtg gaa tgc gag tgt ggc ggc aca aag atc tcc aag acc atc aac	816
Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn	
260 265 270	
aag aca aaa cag ttc agc cag tgc aca aag aag gag cag tgc aga gca	864
Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala	
275 280 285	
tat cgg ctg cag aac gat aag tgg gtg tat aat tct gac aaa ctg ccc	912
Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro	
290 295 300	

0991258-111601

aaa gca gcg gga gcc acc tta aaa gga aaa ctg cat gtc cca ttc ttg 960  
 Lys Ala Ala Gly Ala Thr Leu Lys Gly Lys Leu His Val Pro Phe Leu  
 305 310 315 320

ctg gca gac ggc aaa tgc acc gtg cct cta gca cca gaa cct atg ata 1008  
 Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile  
 325 330 335

acc ttc ggt ttc aga tca gtg tca ctg aaa ctg cac cct aag aat ccc 1056  
 Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro  
 340 345 350

aca tat cta acc acc cgc caa ctt gct gat gag cct cac tac acg cat 1104  
 Thr Tyr Leu Thr Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His  
 355 360 365

gag ctc ata tct gaa cca gct gtt agg aat ttt acc gtc acc gga aaa 1152  
 Glu Leu Ile Ser Glu Pro Ala Val Arg Asn Phe Thr Val Thr Gly Lys  
 370 375 380

ggg tgg gag ttt gta tgg gga aac cac ccg ccg aaa agg ttt tgg gca 1200  
 Gly Trp Glu Phe Val Trp Gly Asn His Pro Pro Lys Arg Phe Trp Ala  
 385 390 395 400

cag gaa aca gca ccc gga aat cca cat ggg cta ccg cac gag gtg ata 1248  
 Gln Glu Thr Ala Pro Gly Asn Pro His Gly Leu Pro His Glu Val Ile  
 405 410 415

act cat tat tac cac aga tac cct atg tcc acc atc ctg ggt ttg tca 1296  
 Thr His Tyr Tyr His Arg Tyr Pro Met Ser Thr Ile Leu Gly Leu Ser  
 420 425 430

att tgt gcc gcc att gca acc gtt tcc gtt gca gcg tct acc tgg ctg 1344  
 Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu  
 435 440 445

ttt tgc aga tct aga gtt gcg tgc cta act cct tac cgg cta aca cct 1392  
 Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro  
 450 455 460

aac gct agg ata cca ttt tgt ctg gct gtg ctt tgc tgc gcc cgc act 1440  
 Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr  
 465 470 475 480

gcc cgg gcc gag acc acc tgg gag tcc ttg gat cac cta tgg aac aat 1488  
 Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn  
 485 490 495

aac caa cag atg ttc tgg att caa ttg ctg atc cct ctg gcc gcc ttg 1536  
 Asn Gln Gln Met Phe Trp Ile Gln Leu Leu Ile Pro Leu Ala Ala Leu  
 500 505 510

atc gta gtg act cgc ctg ctc agg tgc gtg tgc tgt gtc gtg cct ttt 1584  
 Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe  
 515 520 525

0991258 11601

gga gca ttt gga gat ata caa tcc aga aca gtc tca agc tca gat ctg 2256  
Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu  
740 745 750

**00000000000000000000000000000000**

tat gcc aat acc aac cta gtg ctg cag aga ccc aaa gca gga gcg atc	2304
Tyr Ala Asn Thr Asn Leu Val Leu Gln Arg Pro Lys Ala Gly Ala Ile	
755 760 765	
cac gtg cca tac act cag gca cct tcg ggt ttt gag caa tgg aag aaa	2352
His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys	
770 775 780	
gat aaa gct cca tca ttg aaa ttt acc gcc cct ttc gga tgc gaa ata	2400
Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile	
785 790 795 800	
tat aca aac ccc att cgc gcc gaa aac tgt act gta ggg tca att cca	2448
Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro	
805 810 815	
tta gcc ttt gac att ccc gac gcc ttg ttc acc agg gtg tca gaa aca	2496
Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr	
820 825 830	
ccg aca ctt tca gcg gcc gaa tgc act ctt aac gag tgc gtg tat tct	2544
Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser	
835 840 845	
tcc gac ttt ggt ggg atc gcc acg gtc aag tac tcg gcc agc aag tca	2592
Ser Asp Phe Gly Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser	
850 855 860	
ggc aag tgc gca gtc cat gtg cca tca ggg act gct acc cta aaa gaa	2640
Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu	
865 870 875 880	
gca gca gtc gag cta acc gag caa ggg tcg gcg act atc cat ttc tcg	2688
Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser	
885 890 895	
acc gca aat atc cac ccg gag ttc agg ctc caa ata tgc aca tca tat	2736
Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr	
900 905 910	
gtt acg tgc aaa ggt gat tgt cac ccc ccg aaa gac cat att gtg aca	2784
Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr	
915 920 925	
cac cct cag tat cac gcc caa aca ttt aca gcc gcg gtg tca aaa acc	2832
His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr	
930 935 940	
gcg tgg acg tgg tta aca tcc ctg ctg gga gga tca gcc gta att att	2880
Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile	
945 950 955 960	
ata att ggc ttg gtg ctg gct act att gtg gcc atg tac gtg ctg acc	2928
Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr	
965 970 975	

00001258 111601

aac cag aaa cat aat  
 Asn Gln Lys His Asn  
 980

2943

<210> 13  
 <211> 981  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

<400> 13  
 Met Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr Phe Pro  
 1 5 10 15  
 Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu  
 20 25 30  
 Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu  
 35 40 45  
 Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu  
 50 55 60  
 Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile  
 65 70 75 80  
 Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val  
 85 90 95  
 Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln  
 100 105 110  
 Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr  
 115 120 125  
 Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu  
 130 135 140  
 His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu  
 145 150 155 160  
 Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys  
 165 170 175  
 Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn  
 180 185 190  
 Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu  
 195 200 205  
 Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr  
 210 215 220  
 Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser  
 225 230 235 240  
 Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala  
 245 250 255  
 Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn  
 260 265 270  
 Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala  
 275 280 285  
 Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro  
 290 295 300  
 Lys Ala Ala Gly Ala Thr Leu Lys Gly Lys Leu His Val Pro Phe Leu  
 305 310 315 320

09991253-11601



[illegible]

His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys  
 770 775 780  
 Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile  
 785 790 795 800  
 Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro  
 805 810 815  
 Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr  
 820 825 830  
 Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser  
 835 840 845  
 Ser Asp Phe Gly Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser  
 850 855 860  
 Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu  
 865 870 875 880  
 Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser  
 885 890 895  
 Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr  
 900 905 910  
  
 Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr  
 915 920 925  
 His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr  
 930 935 940  
 Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile  
 945 950 955 960  
 Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr  
 965 970 975  
 Asn Gln Lys His Asn  
 980

&lt;210&gt; 14

&lt;211&gt; 12379

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence; Note =  
 synthetic construct

&lt;400&gt; 14

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aggtagaagc	caagcagggt	actgataatg	accatgctaa	tgccagagcg	ttttcgcatc	180
tggcttcaaa	actgatcgaa	acggagggtg	acccatccga	cacgatcctt	gacattggaa	240
gtgcgcccgc	ccgcagaatg	tattctaagc	acaagtatca	ttgtatctgt	ccgatgagat	300
gtgcggaaga	tccggacaga	ttgtataagt	atgcaactaa	gctgaagaaa	aactgtaagg	360
aaataactga	taaggaattg	gacaagaaaa	tgaaggagct	cgccgcccgc	atgagcgacc	420
ctgacctgga	aactgagact	atgtgcctcc	acgacgacga	gtcgtgtcgc	tacgaagggc	480
aagtcgctgt	ttaccaggat	gtatacgcg	ttgacggacc	gacaagtctc	tatcaccaag	540
ccaataagg	agtttagatc	gcctactgga	taggctttga	caccacccct	tttatgttta	600
agaacttggc	tggagcatat	ccatcatact	ctaccaactg	ggccgacgaa	accgtgttaa	660
cggctcgtaa	cataggccta	tgcagctctg	acgttatgga	gcggtcacgt	agagggatgt	720
ccattcttag	aaagaagtat	ttgaaaccat	ccaacaatgt	tctattctct	gttggtcga	780
ccatctacca	cgagaagagg	gacttactga	ggagctggca	cctgccgtct	gtatttcact	840
tacgtggcaa	gcaaaattac	acatgtcgg	gtgagactat	agttagtgtc	gacgggtacg	900
tcgttaaaag	aatagctatc	agtccaggcc	tgtatgggaa	gccttcaggc	tatgctgcta	960
cgatgcaccg	cgagggattc	ttgtgctgca	aagtgcagca	cacattcaac	ggggagaggg	1020

0991258-11601

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<211> 1323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<221> CDS

<222> (1)...(1323)

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atg gat ggc cca aag gtt aaa caa tgg ccg tta aca gaa gtg aaa ata 96  
 Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Val Lys Ile  
 20 25 30

aaa gca tta aca gca att tgt gaa gaa atg gaa aag gaa gga aaa att 144  
 Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu Lys Glu Gly Lys Ile  
 35 40 45

aca aaa att ggg cct gaa aat cca tat aac act cca ata ttc gcc ata 192  
 Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile  
 50 55 60

aaa aag gaa gac agc act aag tgg aga aaa tta gta gat ttc agg gaa 240  
 Lys Lys Glu Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu  
 65 70 75 80

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ctc aat aaa aga act caa gac ttt tgg gag gtt caa tta gga ata cca	288
Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro	
85 90 95	
cac cca gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg gat gtg	336
His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val	
100 105 110	
gga gat gca tat ttt tca gtt cct tta gat gaa ggc ttc agg aaa tat	384
Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr	
115 120 125	
act gca ttc acc ata cct agt ata aac aat gaa aca cca ggg att aga	432
Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg	
130 135 140	
tat caa tat aat gtg ctt cca caa gga tgg aaa ggg tca cca gca ata	480
Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile	
145 150 155 160	
ttc cag gct agc atg aca aaa atc cta gag ccc ttt aga gct aaa aat	528
Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Ala Lys Asn	
165 170 175	
cca gaa ata gtc atc tat caa cat atg gcg gca ttg tat gta gga tct	576
Pro Glu Ile Val Ile Tyr Gln His Met Ala Ala Leu Tyr Val Gly Ser	
180 185 190	
gac tta gaa ata ggg caa cat aga gca aaa ata gaa gag tta aga gaa	624
Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Glu	
195 200 205	
cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat cag aaa	672
His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys	
210 215 220	
gaa ccc cca ttt ctt tgg atg ggg tat gaa ctc cat cct gac aaa tgg	720
Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp	
225 230 235 240	
aca gta cag cct ata cag ctg cca gaa aaa gat agc tgg act gtc aat	768
Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp Ser Trp Thr Val Asn	
245 250 255	
gac ata cag aag tta gtg gga aaa tta aac tgg aca agt cag att tac	816
Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Thr Ser Gln Ile Tyr	
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cca ggg att aaa gta agg caa ctt tgt aag ctc ctt agg ggg acc aaa	864
Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys	
275 280 285	
gca cta aca gac ata gta cca cta act gaa gaa gca gaa tta gaa ttg	912
Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu	
290 295 300	

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gca gag aac agg gaa att cta aaa gaa cca gtg cat gga gta tat tat 960  
Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr  
305 310 315 320

gac cca tca aaa gac ttg ata gct gaa ata cag aaa cag ggg gat gac 1008  
Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Asp Asp  
325 330 335

caa tgg aca tat caa att tac caa gaa cca ttc aaa aac ctg aag aca 1056  
Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr  
340 345 350

gga aag tat gca aaa agg agg act acc cac act aat gat gta aaa cag 1104  
Gly Lys Tyr Ala Lys Arg Arg Thr Thr His Thr Asn Asp Val Lys Gln  
355 360 365

tta aca gag gca gtg caa aaa ata tcc ttg gaa agc ata gta aca tgg 1152  
Leu Thr Glu Ala Val Gln Lys Ile Ser Leu Glu Ser Ile Val Thr Trp  
370 375 380

gga aag act cct aaa ttt aga cta ccc atc caa aaa gaa aca tgg gaa 1200  
Gly Lys Thr Pro Lys Phe Arg Leu Pro Ile Gln Lys Glu Thr Trp Glu  
385 390 395 400

ata tgg tgg aca gac tat tgg caa gcc aca tgg att cct gag tgg gag 1248  
Ile Trp Trp Thr Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu  
405 410 415

ttt gtt aat acc cct ccc cta gta aaa cta tgg tac cag cta gaa aaa 1296  
Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys  
420 425 430

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<210> 16

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 16

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20 25 30  
Lys Ala Leu Thr Ala Ile Cys Glu Met Glu Lys Glu Gly Lys Ile  
35 40 45  
Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile  
50 55 60  
Lys Lys Glu Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu  
65 70 75 80

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Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro  
 85 90 95  
 His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val  
 100 105 110  
 Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr  
 115 120 125  
 Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg  
 130 135 140  
  
 Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile  
 145 150 155 160  
 Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Ala Lys Asn  
 165 170 175  
 Pro Glu Ile Val Ile Tyr Gln His Met Ala Ala Leu Tyr Val Gly Ser  
 180 185 190  
 Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Glu  
 195 200 205  
 His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys  
 210 215 220  
 Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp  
 225 230 235 240  
 Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp Ser Trp Thr Val Asn  
 245 250 255  
 Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Thr Ser Gln Ile Tyr  
 260 265 270  
 Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys  
 275 280 285  
 Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu  
 290 295 300  
 Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr  
 305 310 315 320  
 Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Asp Asp  
 325 330 335  
 Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr  
 340 345 350  
  
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&lt;220&gt;

 <223> Description of Artificial Sequence; Note =  
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gctcttccgc	ttcctcgctc	actgaactgc	tgcgctcggt	cgttcggctg	cggcgagcgg	11760
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agaacatgtg	agcaaaaggc	cagcaaaagg	ccaggaaacc	taaaaaggcc	gcgttgctgg	11880
cgtttttcca	taggctccgc	ccccctgacg	agcatcacaa	aaatcgacgc	tcaagtcaga	11940
ggtggcgaaa	cccgcagagga	ctataaagat	accaggcggt	ttccccctgga	agctccctcg	12000
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gaagcgtggc	gctttctcat	agctcaacgt	gtaggatatc	cagttcggtg	taggtcggtc	12120
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ggcctaacta	cggctacact	agaaggacag	tatttggtat	ctgcgctctg	ctgaagccag	12360
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ctttgatctt	ttctacgggg	tctgacgctc	agtggaaacga	aaactcacgt	taagggattt	12540
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catattcaac	gggaaacgtc	ttgctcgagg	ccgcgattaa	attccaacat	ggatgctgat	12660
ttatatgggt	ataaatgggc	tcgcgataat	gtcgggcaat	caggtgcgac	aatctatcga	12720
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aatgatgtta	cagatgagat	ggtcagacta	aactggctga	cggaatttat	gcctcttccg	12840
accatcaagc	atthttatccg	tactcctgat	gatgcattgt	tactcaccac	tgcatcccc	12900
gggaaaacag	cattccaggt	attagaagaa	tactctgatt	caggtgaaaa	tattgttgat	12960
gcgctggcag	tgttcctgcg	ccggttgcat	tcgattcctg	tttgtaattg	tccttttaac	13020
agcgatcgcg	tatttcgtct	cgctcaggcg	caatcacgaa	tgaataacgg	tttggttgat	13080
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aaccttattt	ttgacgaggg	gaaattaata	ggttgatttg	atgttgagcg	agtcggaatc	13260
gcagaccgat	accaggatct	tgccatccta	tgggaactgcc	tcggtgagtt	ttctccttca	13320
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tttcatttga	tgctcgatga	gtttttctaa	gaattctcat	gtttgacagc	ttatcatcga	13440
taagctttta	tgcggtagtt	tatcacagtt	aaattgctaa	cgcagtcagg	caccgtgtat	13500
gaaatctaac	aatgcgctca	tcgtcactct	cggcaccgtc	accctggatg	ctgtctagag	13560
gatccctaac	acgactcact	atag				13584

09991253.111601

<210> 18  
 <211> 2532  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
 synthetic construct

<221> CDS

<222> (1)...(2532)

<400> 18

atg aga gtg atg ggg ata cag agg aat tgg cca caa tgg tgg ata tgg 48  
 Met Arg Val Met Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp  
 1 5 10 15

ggc acc tta ggc ttt tgg atg ata ata att tgt agg gtg gtg ggg aac 96  
 Gly Thr Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Val Gly Asn  
 20 25 30

ttg aac ttg tgg gtc aca gtc tat tat ggg gta cct gtg tgg aaa gaa 144  
 Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu  
 35 40 45

gca aaa act act cta ttc tgt gca tca gat gct aaa gca tat gat aaa 192  
 Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys  
 50 55 60

gaa gta cat aat gtc tgg gct aca cat gcc tgt gta ccc aca gac ccc 240  
 Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro  
 65 70 75 80

aac cca cga gaa ata gtt ttg gaa aat gta aca gaa aat ttt aac atg 288  
 Asn Pro Arg Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met  
 85 90 95

tgg aaa aat gac atg gtg gat cag atg cat gag gat ata atc agt tta 336  
 Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu  
 100 105 110

tgg gat caa agc cta aaa cca tgt gta aag ttg acc cca ctc tgt gtc 384  
 Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val  
 115 120 125

act tta aat tgt aca aat gca cct gcc tac aat aat agc atg cat gga 432  
 Thr Leu Asn Cys Thr Asn Ala Pro Ala Tyr Asn Asn Ser Met His Gly  
 130 135 140

gaa atg aaa aat tgc tct ttc aat aca acc aca gag ata aga gat agg 480  
 Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg Asp Arg  
 145 150 155 160

aaa cag aaa gcg tat gca ctt ttt tat aaa cct gat gta gtg cca ctt 528  
 Lys Gln Lys Ala Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu  
 165 170 175

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aat agg aga gaa gag aat aat ggg aca gga gag tat ata tta ata aat	576
Asn Arg Arg Glu Glu Asn Asn Gly Thr Gly Glu Tyr Ile Leu Ile Asn	
180 185 190	
tgc aat tcc tca acc ata aca caa gcc tgt cca aag gtc act ttt gac	624
Cys Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Thr Phe Asp	
195 200 205	
cca att cct ata cat tat tgt gct cca gct ggt tat gcg att cta aag	672
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys	
210 215 220	
tgt aat aat aag aca ttc aat ggg aca gga cca tgc aat aat gtc agc	720
Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser	
225 230 235 240	
aca gta caa tgt aca cat gga att atg cca gtg gta tca act caa tta	768
Thr Val Gln Cys Thr His Gly Ile Met Pro Val Val Ser Thr Gln Leu	
245 250 255	
ctg tta aat ggt agc cta gca gaa gaa gag ata ata att aga tct gaa	816
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Ile Arg Ser Glu	
260 265 270	
aat ctg aca aac aat atc aaa aca ata ata gtc cac ctt aat aaa tct	864
Asn Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser	
275 280 285	
gta gaa att gtg tgt aca aga ccc aac aat aat aca aga aaa agt ata	912
Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile	
290 295 300	
agg ata gga cca gga caa aca ttc tat gca aca ggt gaa ata ata gga	960
Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly	
305 310 315 320	
aac ata aga gaa gca cat tgt aac att agt aaa agt aac tgg acc agt	1008
Asn Ile Arg Glu Ala His Cys Asn Ile Ser Lys Ser Asn Trp Thr Ser	
325 330 335	
act tta gaa cag gta aag aaa aaa tta aaa gaa cac tac aat aag aca	1056
Thr Leu Glu Gln Val Lys Lys Lys Leu Lys Glu His Tyr Asn Lys Thr	
340 345 350	
ata gaa ttt aac cca ccc tca gga ggg gat cta gaa gtt aca aca cat	1104
Ile Glu Phe Asn Pro Pro Ser Gly Gly Asp Leu Glu Val Thr Thr His	
355 360 365	
agc ttt aat tgt aga gga gaa ttt ttc tat tgc aat aca aca aaa ctg	1152
Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu	
370 375 380	
ttt tca aac aac agt gat tca aac aac gaa acc atc aca ctc cca tgc	1200
Phe Ser Asn Asn Ser Asp Ser Asn Asn Glu Thr Ile Thr Leu Pro Cys	
385 390 395 400	

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aag ata aaa caa att ata aac atg tgg cag aag gta gga cga gca atg	1248
Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met	
405 410 415	
tat gcc cct ccc att gaa gga aac ata aca tgt aaa tca aat atc aca	1296
Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr	
420 425 430	
gga cta cta ttg aca cgt gat gga gga aag aat aca aca aat gag ata	1344
Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile	
435 440 445	
ttc aga ccg gga gga gga aat atg aag gac aat tgg aga agt gaa tta	1392
Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu	
450 455 460	
tat aaa tat aaa gtg gta gaa att gag cca ttg gga gta gca ccc act	1440
Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr	
465 470 475 480	
aaa tca aaa agg aga gtg gtg gag aga gaa aaa aga gca gtg gga cta	1488
Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu	
485 490 495	
gga gct gta ctc ctt ggg ttc ttg gga gca gca gga agc act atg ggc	1536
Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly	
500 505 510	
gcg gcg tca ata acg ctg acg gta cag gcc aga caa ctg ttg tct ggt	1584
Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly	
515 520 525	
ata gtg caa cag caa agc aat ttg ctg aga gct ata gag gcg caa cag	1632
Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln	
530 535 540	
cat atg ttg caa ctc acg gtc tgg ggc att aag cag ctc cag aca aga	1680
<del>His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg</del>	
<del>545 550 555 560</del>	
gtc ttg gct ata gag aga tac cta aag gat caa cag ctc cta ggg ctt	1728
Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu	
565 570 575	
tgg ggc tgc tct gga aaa atc atc tgc acc act gct gtg cct tgg aac	1776
Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn	
580 585 590	
tcc agt tgg agt aat aaa tct caa gaa gat att tgg gat aac atg acc	1824
Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr	
595 600 605	
tgg atg cag tgg gat aga gaa att agt aat tac aca ggc aca ata tat	1872
Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr	
610 615 620	

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agg tta ctt gaa gac tcg caa aac cag cag gag aaa aat gaa aaa gat	1920
Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp	
625 630 635 640	
tta tta gca ttg gac agt tgg aaa aac ttg tgg aat tgg ttt aac ata	1968
Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile	
645 650 655	
aca aat tgg ctg tgg tat ata aaa ata ttc atc atg ata gta gga ggc	2016
Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly	
660 665 670	
ttg ata ggt ttg aga ata att ttt ggt gta ctc gct ata gtg aaa aga	2064
Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg	
675 680 685	
gtt agg cag gga tac tca cct ttg tcg ttt cag acc ctt acc cca agc	2112
Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser	
690 695 700	
ccg agg ggt ccc gac agg ctc gga aga atc gaa gaa gaa ggt gga gag	2160
Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu	
705 710 715 720	
caa gac aaa gac aga tcc att cga tta gtg agc gga ttc tta gca ctt	2208
Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu	
725 730 735	
gcc tgg gac gat ctg cgg agc ctg tgc ctc ttc agc tac cac cac ttg	2256
Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu	
740 745 750	
aga gac ttc ata ttg att gca gcg aga gca gcg gaa ctt ctg gga cgc	2304
Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg	
755 760 765	
agc agt ctc agg gga ctg cag aga ggg tgg gaa gcc ctt aag tat ctg	2352
Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu	
770 775 780	
gga aat ctt gtg cag tat ggg ggt ctg gag cta aaa aga agt gct att	2400
Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile	
785 790 795 800	
aaa ctg ttt gat acc ata gca ata gca gta gct gaa gga aca gat agg	2448
Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg	
805 810 815	
att ctt gaa gta ata cag aga att tgt aga gct atc cgc cac ata cct	2496
Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro	
820 825 830	
ata aga ata aga cag ggc ttt gaa gca gct ttg caa	2532
Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln	
835 840	

&lt;211&gt; 844

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;400&gt; 19

Met	Arg	Val	Met	Gly	Ile	Gln	Arg	Asn	Trp	Pro	Gln	Trp	Trp	Ile	Trp	1	5	10	15
Gly	Thr	Leu	Gly	Phe	Trp	Met	Ile	Ile	Ile	Cys	Arg	Val	Val	Gly	Asn	20	25	30	
Leu	Asn	Leu	Trp	Val	Thr	Val	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu		35	40	45	
Ala	Lys	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Lys	50	55	60	
Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	65	70	75	80
Asn	Pro	Arg	Glu	Ile	Val	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	85	90	95	
Trp	Lys	Asn	Asp	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	100	105	110	
Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	115	120	125	
Thr	Leu	Asn	Cys	Thr	Asn	Ala	Pro	Ala	Tyr	Asn	Asn	Ser	Met	His	Gly	130	135	140	
Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Thr	Thr	Thr	Glu	Ile	Arg	Asp	Arg	145	150	155	160
Lys	Gln	Lys	Ala	Tyr	Ala	Leu	Phe	Tyr	Lys	Pro	Asp	Val	Val	Pro	Leu	165	170	175	
Asn	Arg	Arg	Glu	Asn	Asn	Gly	Thr	Gly	Glu	Tyr	Ile	Leu	Ile	Asn		180	185	190	
Cys	Asn	Ser	Ser	Thr	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Thr	Phe	Asp	195	200	205	
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	210	215	220	
Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	225	230	235	240
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Met	Pro	Val	Val	Ser	Thr	Gln	Leu	245	250	255	
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	260	265	270	
Asn	Leu	Thr	Asn	Asn	Ile	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Lys	Ser	275	280	285	
Val	Glu	Ile	Val	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	290	295	300	
Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	305	310	315	320
Asn	Ile	Arg	Glu	Ala	His	Cys	Asn	Ile	Ser	Lys	Ser	Asn	Trp	Thr	Ser	325	330	335	
Thr	Leu	Glu	Gln	Val	Lys	Lys	Lys	Leu	Lys	Glu	His	Tyr	Asn	Lys	Thr	340	345	350	
Ile	Glu	Phe	Asn	Pro	Pro	Ser	Gly	Gly	Asp	Leu	Glu	Val	Thr	Thr	His	355	360	365	

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Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu  
 370 375 380  
 Phe Ser Asn Asn Ser Asp Ser Asn Asn Glu Thr Ile Thr Leu Pro Cys  
 385 390 395 400  
 Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met  
 405 410 415  
 Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr  
 420 425 430  
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile  
 435 440 445  
 Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu  
 450 455 460  
 Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr  
 465 470 475 480  
 Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu  
 485 490 495  
 Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly  
 500 505 510  
 Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly  
 515 520 525  
 Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln  
 530 535 540  
 His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg  
 545 550 555 560  
 Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu  
 565 570 575  
 Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn  
 580 585 590  
 Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr  
 595 600 605  
 Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr  
 610 615 620  
 Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp  
 625 630 635 640  
 Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile  
 645 650 655  
 Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly  
 660 665 670  
 Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg  
 675 680 685  
 Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser  
 690 695 700  
 Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Glu  
 705 710 715 720  
 Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu  
 725 730 735  
 Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu  
 740 745 750  
 Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Gly Arg  
 755 760 765  
 Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu  
 770 775 780  
 Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile  
 785 790 795 800  
 Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg  
 805 810 815

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ATTORNEY DOCKET NO. 01113.0001U3

Ile	Leu	Glu	Val	Ile	Gln	Arg	Ile	Cys	Arg	Ala	Ile	Arg	His	Ile	Pro
			820					825					830		
Ile	Arg	Ile	Arg	Gln	Gly	Phe	Glu	Ala	Ala	Leu	Gln				
		835					840								

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